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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/989,350

DATE: 01/26/2002

TIME: 13:47:25

Input Set : N:\Crf3\RULE60\09989350.raw

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1 <110> APPLICANT: Lin, Lih-Ling
 2 Chen, Jennifer H.
 3 Schievella, Andrea
 4 Graham, James
 5 <120> TITLE OF INVENTION: Novel TNF receptor death domain ligand proteins and
 6 inhibitors of ligand binding(as amended)
 7 <130> FILE REFERENCE: GFN-5232CP4DV3
 8 <140> CURRENT APPLICATION NUMBER: US/09/989,350
 9 <141> CURRENT FILING DATE: 2001-11-20
 10 <150> PRIOR APPLICATION NUMBER: 09/185,258
 11 <151> PRIOR FILING DATE: 1998-11-02
 12 <150> PRIOR APPLICATION NUMBER: 08/839,032
 13 <151> PRIOR FILING DATE: 1997-04-23
 14 <150> PRIOR APPLICATION NUMBER: 08/698,551
 15 <151> PRIOR FILING DATE: 1996-08-15
 16 <150> PRIOR APPLICATION NUMBER: 08/602,228
 17 <151> PRIOR FILING DATE: 1996-02-15
 18 <150> PRIOR APPLICATION NUMBER: 08/533,901
 19 <151> PRIOR FILING DATE: 1995-09-26
 20 <150> PRIOR APPLICATION NUMBER: 08/494,440
 21 <151> PRIOR FILING DATE: 1995-06-19
 22 <150> PRIOR APPLICATION NUMBER: 08/327,514
 23 <151> PRIOR FILING DATE: 1994-10-19
 24 <160> NUMBER OF SEQ ID NOS: 19
 25 <170> SOFTWARE: PatentIn Ver. 2.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 2158
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
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 37 1 5 10 15
 38 agc tct cgg ggc act ttg tct gat agt gaa att gag acc aac tct gcc 97
 39 Ser Ser Arg Gly Thr Leu Ser Asp Ser Glu Ile.Glu Thr Asn Ser Ala
 40 20 25 30
 41 aca agc acc atc ttt ggt aaa gcc cac agc ttg aag cca agc ata aag 145
 42 Thr Ser Thr Ile Phe Gly Lys Ala His Ser Leu Lys Pro Ser Ile Lys
 43 35 40 45
 44 gag aag ctg gca ggc agc ccc att cgt act tct gaa gat gtg agc cag 193

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47	cga gtc tat ctc tat gag gga ctc cta ggc aaa gag cgt tct act tta	241
48	Arg Val Tyr Leu Tyr Glu Gly Leu Leu Gly Lys Glu Arg Ser Thr Leu	
49	65 70 75 80	
50	tgg gac caa atg caa ttc tgg gaa gat gcc ttc tta gat gct gtg atg	289
51	Trp Asp Gln Met Gln Phe Trp Glu Asp Ala Phe Leu Asp Ala Val Met	
52	85 90 95	
53	ttg gag aga gaa ggg atg ggt atg gac cag ggt ccc cag gaa atg atc	337
54	Leu Glu Arg Glu Gly Met Gly Met Asp Gln Gly Pro Gln Glu Met Ile	
55	100 105 110	
56	gac agg tac ctg tcc ctt gga gaa cat gac cgg aag cgc ctg gaa gat	385
57	Asp Arg Tyr Leu Ser Leu Gly Glu His Asp Arg Lys Arg Leu Glu Asp	
58	115 120 125	
59	gat gaa gat cgc ttg ctg gcc aca ctt ctg cac aac ctc atc tcc tac	433
60	Asp Glu Asp Arg Leu Leu Ala Thr Leu Leu His Asn Leu Ile Ser Tyr	
61	130 135 140	
62	atg ctg ctg atg aag gta aat aag aat gac atc cgc aag aag gtg agg	481
63	Met Leu Leu Met Lys Val Asn Lys Asn Asp Ile Arg Lys Lys Val Arg	
64	145 150 155 160	
65	cgc cta atg gga aag tcg cac att ggg ctt gtg tac agc cag caa atc	529
66	Arg Leu Met Gly Lys Ser His Ile Gly Leu Val Tyr Ser Gln Gln Ile	
67	165 170 175	
68	aat gag gtg ctt gat cag ctg gcg aac ctg aat gga cgc gat ctc tct	577
69	Asn Glu Val Leu Asp Gln Leu Ala Asn Leu Asn Gly Arg Asp Leu Ser	
70	180 185 190	
71	atc tgg tcc agt ggc agc cgg cac atg aag aag cag aca ttt gtg gta	625
72	Ile Trp Ser Ser Gly Ser Arg His Met Lys Lys Gln Thr Phe Val Val	
73	195 200 205	
74	cat gca ggg aca gat aca aac gga gat atc ttt ttc atg gag gtg tgc	673
75	His Ala Gly Thr Asp Thr Asn Gly Asp Ile Phe Phe Met Glu Val Cys	
76	210 215 220	
77	gat gac tgt gtg gtg ttg cgt agt aac atc gga aca gtg tat gag cgc	721
78	Asp Asp Cys Val Val Leu Arg Ser Asn Ile Gly Thr Val Tyr Glu Arg	
79	225 230 235 240	
80	tgg tgg tac gag aag ctc atc aac atg acc tac tgt ccc aag acg aag	769
81	Trp Trp Tyr Glu Lys Leu Ile Asn Met Thr Tyr Cys Pro Lys Thr Lys	
82	245 250 255	
83	gtg ttg tgc ttg tgg cgt aga aat ggc tct gag acc cag ctc aac aag	817
84	Val Leu Cys Leu Trp Arg Arg Asn Gly Ser Glu Thr Gln Leu Asn Lys	
85	260 265 270	
86	ttc tat act aaa aag tgt cgg gag ctg tac tac tgt gtg aag gac agc	865
87	Phe Tyr Thr Lys Lys Cys Arg Glu Leu Tyr Tyr Cys Val Lys Asp Ser	
88	275 280 285	
89	atg gag cgc gct gcc gcc cga cag caa agc atc aaa ccc gga cct gaa	913
90	Met Glu Arg Ala Ala Ala Arg Gln Gln Ser Ile Lys Pro Gly Pro Glu	
91	290 295 300	
92	ttg ggt ggc gag ttc cct gtg cag gac ctg aag act ggt gag ggt ggc	961
93	Leu Gly Gly Glu Phe Pro Val Gln Asp Leu Lys Thr Gly Glu Gly Gly	

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96      Leu Leu Gln Val Thr Leu Glu Gly Ile Asn Leu Lys Phe Met His Asn
97      325      330      335
98      cag gtt ttc ata gag ctg aat cac att aaa aag tgc aat aca gtt cga 1057
99      Gln Val Phe Ile Glu Leu Asn His Ile Lys Lys Cys Asn Thr Val Arg
100     340      345      350
101     ggc gtc ttt gtc ctg gag gaa ttt gtt cct gaa att aaa gaa gtc gtc 1105
102     Gly Val Phe Val Leu Glu Glu Phe Val Pro Glu Ile Lys Glu Val Val
103     355      360      365
104     agc cac aag tac aag aca cca atg gcc cac gaa atc tgc tac tcc gta 1153
105     Ser His Lys Tyr Lys Thr Pro Met Ala His Glu Ile Cys Tyr Ser Val
106     370      375      380
107     tta tgt ctc ttc tcg tac gtg gct gca gtt cat agc agt gag gaa gat 1201
108     Leu Cys Leu Phe Ser Tyr Val Ala Ala Val His Ser Ser Glu Glu Asp
109     385      390      395      400
110     ctc aga acc ccg ccc cgg cct gtc tct agc tgatggagag gggctacgca 1251
111     Leu Arg Thr Pro Pro Arg Pro Val Ser Ser
112     405      410
113     gctgccccag cccagggcac gcccttgccc ccttgctgtt cccaagtgca cgatgctgct 1311
114     gtgactgagg agtggatgat gctcgtgtgt cctctgcaag cccctgctg tggcttgggt 1371
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117     cggtgtgaac ccactatttt gtgtccttga gacatttgtg ttgtgggttc ttgtccttgt 1551
118     ccctggcggt aactgtccac tgcaagagtc tggctctccc ttctctgtga cccggcatga 1611
119     ctgggcgcct ggagcagttt cactctgtga ggagtgaagg aacctggggg ctcacctctt 1671
120     cagaggaagg gcacagagag gaagggaaga attggggggc agccggagtg agtggcagcc 1731
121     tccctgcttc cttctgcatt cccaagccgg cagctactgc ccagggcccg cagtgttggc 1791
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123     gccttcggca tcagaggatg gagtggtcga ggctagtggg gtcccaggga ccgctggctg 1911
124     ctctgcctga gcatcaggga gggggcagga aagaccaagc tgggtttgca catctgtctg 1971
125     caggctgtct ctccaggcac ggggtgtcag gagggagaga cagcctgggt atgggcaaga 2031
126     aatgactgta aatatttcag cccacatta tttatagaaa atgtacagtt gtgtgaatgt 2091
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138     20      25      30
139     Thr Ser Thr Ile Phe Gly Lys Ala His Ser Leu Lys Pro Ser Ile Lys
140     35      40      45
141     Glu Lys Leu Ala Gly Ser Pro Ile Arg Thr Ser Glu Asp Val Ser Gln
142     50      55      60
143     Arg Val Tyr Leu Tyr Glu Gly Leu Leu Gly Lys Glu Arg Ser Thr Leu

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147	Leu Glu Arg Glu Gly Met Gly Met Asp Gln Gly Pro Gln Glu Met Ile			
148		100	105	110
149	Asp Arg Tyr Leu Ser Leu Gly Glu His Asp Arg Lys Arg Leu Glu Asp			
150		115	120	125
151	Asp Glu Asp Arg Leu Leu Ala Thr Leu Leu His Asn Leu Ile Ser Tyr			
152		130	135	140
153	Met Leu Leu Met Lys Val Asn Lys Asn Asp Ile Arg Lys Lys Val Arg			
154		145	150	155
155	Arg Leu Met Gly Lys Ser His Ile Gly Leu Val Tyr Ser Gln Gln Ile			
156		165	170	175
157	Asn Glu Val Leu Asp Gln Leu Ala Asn Leu Asn Gly Arg Asp Leu Ser			
158		180	185	190
159	Ile Trp Ser Ser Gly Ser Arg His Met Lys Lys Gln Thr Phe Val Val			
160		195	200	205
161	His Ala Gly Thr Asp Thr Asn Gly Asp Ile Phe Phe Met Glu Val Cys			
162		210	215	220
163	Asp Asp Cys Val Val Leu Arg Ser Asn Ile Gly Thr Val Tyr Glu Arg			
164		225	230	235
165	Trp Trp Tyr Glu Lys Leu Ile Asn Met Thr Tyr Cys Pro Lys Thr Lys			
166		245	250	255
167	Val Leu Cys Leu Trp Arg Arg Asn Gly Ser Glu Thr Gln Leu Asn Lys			
168		260	265	270
169	Phe Tyr Thr Lys Lys Cys Arg Glu Leu Tyr Tyr Cys Val Lys Asp Ser			
170		275	280	285
171	Met Glu Arg Ala Ala Ala Arg Gln Gln Ser Ile Lys Pro Gly Pro Glu			
172		290	295	300
173	Leu Gly Gly Glu Phe Pro Val Gln Asp Leu Lys Thr Gly Glu Gly Gly			
174		305	310	315
175	Leu Leu Gln Val Thr Leu Glu Gly Ile Asn Leu Lys Phe Met His Asn			
176		325	330	335
177	Gln Val Phe Ile Glu Leu Asn His Ile Lys Lys Cys Asn Thr Val Arg			
178		340	345	350
179	Gly Val Phe Val Leu Glu Glu Phe Val Pro Glu Ile Lys Glu Val Val			
180		355	360	365
181	Ser His Lys Tyr Lys Thr Pro Met Ala His Glu Ile Cys Tyr Ser Val			
182		370	375	380
183	Leu Cys Leu Phe Ser Tyr Val Ala Ala Val His Ser Ser Glu Glu Asp			
184		385	390	395
185	Leu Arg Thr Pro Pro Arg Pro Val Ser Ser			
186		405	410	

188 <210> SEQ ID NO: 3

189 <211> LENGTH: 826

190 <212> TYPE: DNA

191 <213> ORGANISM: Homo sapiens

192 <220> FEATURE:

193 <221> NAME/KEY: CDS

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Input Set : N:\Crf3\RULE60\09989350.raw

Output Set: N:\CRF3\01252002\I989350.raw

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199   ctg gtg ctg tac agt gga gag gat gat gag ctg cta cag cgg gca gct 97
200   Leu Val Leu Tyr Ser Gly Glu Asp Asp Glu Leu Leu Gln Arg Ala Ala
201       20           25           30
202   gcc ggg ggc ttg gcc atg ctt acc tcc atg cgg ccc acg ctc tgc agc 145
203   Ala Gly Gly Leu Ala Met Leu Thr Ser Met Arg Pro Thr Leu Cys Ser
204       35           40           45
205   cgc att ccc caa gtg acc aca cac tgg ctg gag atc ctg cag gcc ctg 193
206   Arg Ile Pro Gln Val Thr Thr His Trp Leu Glu Ile Leu Gln Ala Leu
207       50           55           60
208   ctt ctg agc tcc aac cag gag ctg cag cac cgg ggt gct gtg gtg gtg 241
209   Leu Leu Ser Ser Asn Gln Glu Leu Gln His Arg Gly Ala Val Val Val
210       65           70           75           80
211   ctg aac atg gtg gag gcc tgc agg gag att gcc agc acc ctg atg gag 289
212   Leu Asn Met Val Glu Ala Ser Arg Glu Ile Ala Ser Thr Leu Met Glu
213       85           90           95
214   agt gag atg atg gag atc ttg tca gtg cta gct aag ggt gac cac agc 337
215   Ser Glu Met Met Glu Ile Leu Ser Val Leu Ala Lys Gly Asp His Ser
216       100          105          110
217   cct gtc aca agg gct gct gca gcc tgc ctg gac aaa gca gtg gaa tat 385
218   Pro Val Thr Arg Ala Ala Ala Cys Leu Asp Lys Ala Val Glu Tyr
219       115          120          125
220   ggg ctt atc caa ccc aac caa gat gga gag tgaggggggtt gtccctgggc 435
221   Gly Leu Ile Gln Pro Asn Gln Asp Gly Glu
222       130          135
223   ccaaggctca tgcacacgct acctattgtg gcacggagag taaggacgga agcagctttg 495
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225   cctctgttct gagtcagcgg ccacgttcag tcacacagcc ctgcttggcc agcactgcct 615
226   gcagcctcac tcagagggggc cctttttctg tactactgta gtcagctggg aatggggaag 675
227   gtgcatccca acacagcctg tggatcctgg ggcatttgga agggcgca caatcagcagc 735
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239       20           25           30
240   Ala Gly Gly Leu Ala Met Leu Thr Ser Met Arg Pro Thr Leu Cys Ser
241       35           40           45
242   Arg Ile Pro Gln Val Thr Thr His Trp Leu Glu Ile Leu Gln Ala Leu
243       50           55           60

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